



SEQUENCE LISTING

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(1) GENERAL INFORMATION:

- (i) APPLICANT: Inze, Dirk  
De Veylder Lieven  
De Almeida Janice
- (ii) TITLE OF INVENTION: A novel mitogenic cyclin and uses thereof
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS
  - (A) ADDRESSEE: Nixon Peabody LLP
  - (B) STREET: 990 Stewart Avenue
  - (C) CITY: Garden City
  - (D) STATE: New York, New York
  - (E) ZIP: 11530
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/530,209
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: EP PCT/EP98/06749
  - (B) FILING DATE: 23-OCT-1998
  - (A) APPLICATION NUMBER: EP 97.203.303.9
  - (B) FILING DATE: 24-OCT-1997

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 927 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..927
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG GCA GAG GAA AAT CTA GAA CTG AGT CTT TTA TGT ACA GAG AGC AAC  
Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn  
1 5 10 15

GTT GAT GAT GAG GGC ATG ATT GTT GAC GAA ACT CCG ATT GAA ATT TCG	96
Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser	
20 25 30	
ATT CCT CAG ATG GGT TTT TCT CAA TCG GAG AGT GAG GAG ATT ATC ATG	144
Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met	
35 40 45	
GAG ATG GTG GAG AAG GAG AAG CAG CAT TTG CCA AGT GAT GAT TAC ATC	192
Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile	
50 55 60	
AAG AGA CTT AGA AGT GGA GAT TTG GAT TTG AAT GTT GGA AGA AGA GAT	240
Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp	
65 70 75 80	
GCC CTC AAT TGG ATT TGG AAG GCT TGT GAA GTA CAC CAG TTT GGA CCA	288
Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro	
85 90 95	
TTG TGT TTT TGC TTA GCA ATG AAC TAC TTG GAT CGA TTC TTA TCG GTT	336
Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val	
100 105 110	
CAT GAT TTG CCT AGT GGC AAA GGT TGG ATA TTG CAG TTG TTG GCT GTG	384
His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val	
115 120 125	
GCT TGT TTA TCA TTG GCA GCC AAA ATT GAA GAA ACT GAA GTT CCA ATG	432
Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met	
130 135 140	
TTG ATA GAT CTT CAG GTT GGA GAT CCT CAG TTT GTG TTT GAG GCT AAA	480
Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys	
145 150 155 160	
TCA GTC CAA AGA ATG GAG CTT TTG GTG TTG AAC AAA TTG AAA TGG AGA	528
Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arg	
165 170 175	
TTG AGA GCA ATA ACT CCA TGC TCA TAC ATA AGA TAT TTC CTG AGA AAG	576
Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys	
180 185 190	
ATG AGT AAA TGT GAT CAA GAA CCA TCC AAC ACA TTG ATA TCT AGA TCA	624
Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser	
195 200 205	
TTA CAA GTG ATA GCC AGC ACA ACC AAA GGT ATT GAC TTT TTG GAG TTT	672
Leu Gln Val Ile Ala Ser Thr Lys Gly Ile Asp Phe Leu Glu Phe	
210 215 220	
AGA CCT TCT GAA GCT GCT GCT GCT GTG GCA CTT TCT GTT TCT GGA GAA	720
Arg Pro Ser Glu Ala Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu	
225 230 235 240	
TTG CAG AGA GTA CAC TTT GAC AAC TCT TCC TTC TCT CCT CTT TTC TCA	768
Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser	
245 250 255	

CTA CTT CAA AAG GAG AGA GTG AAG AAG ATA GGG GAA ATG ATA GAG AGT	816
Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser	
260 265 270	
GAT GGC TCA GAC TTA TGT TCA CAA ACA CCC AAT GGG GTT TTA GAA GTA	864
Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val	
275 280 285	
TCG GCT TGT TGT TTC AGC TTT AAG ACC CAT GAT TCT TCT TCT TCT TAT	912
Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr	
290 295 300	
ACA CAT CTT TCT TAA	927
Thr His Leu Ser	
305	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Glu	Glu	Asn	Leu	Glu	Leu	Ser	Leu	Leu	Cys	Thr	Glu	Ser	Asn	
1				5				10						15		
Val	Asp	Asp	Glu	Gly	Met	Ile	Val	Asp	Glu	Thr	Pro	Ile	Glu	Ile	Ser	
			20					25					30			
Ile	Pro	Gln	Met	Gly	Phe	Ser	Gln	Ser	Glu	Ser	Glu	Glu	Ile	Ile	Met	
			35				40					45				
Glu	Met	Val	Glu	Lys	Glu	Lys	Gln	His	Leu	Pro	Ser	Asp	Asp	Tyr	Ile	
	50					55					60					
Lys	Arg	Leu	Arg	Ser	Gly	Asp	Leu	Asp	Leu	Asn	Val	Gly	Arg	Arg	Asp	
65					70					75					80	
Ala	Leu	Asn	Trp	Ile	Trp	Lys	Ala	Cys	Glu	Val	His	Gln	Phe	Gly	Pro	
				85					90					95		
Leu	Cys	Phe	Cys	Leu	Ala	Met	Asn	Tyr	Leu	Asp	Arg	Phe	Leu	Ser	Val	
			100				105						110			
His	Asp	Leu	Pro	Ser	Gly	Lys	Gly	Trp	Ile	Leu	Gln	Leu	Leu	Ala	Val	
		115					120					125				
Ala	Cys	Leu	Ser	Leu	Ala	Ala	Lys	Ile	Glu	Glu	Thr	Glu	Val	Pro	Met	
	130					135					140					
Leu	Ile	Asp	Leu	Gln	Val	Gly	Asp	Pro	Gln	Phe	Val	Phe	Glu	Ala	Lys	
145					150					155					160	
Ser	Val	Gln	Arg	Met	Glu	Leu	Leu	Val	Leu	Asn	Lys	Leu	Lys	Trp	Arg	

165										170					175				
Leu	Arg	Ala	Ile	Thr	Pro	Cys	Ser	Tyr	Ile	Arg	Tyr	Phe	Leu	Arg	Lys				
			180					185					190						
Met	Ser	Lys	Cys	Asp	Gln	Glu	Pro	Ser	Asn	Thr	Leu	Ile	Ser	Arg	Ser				
		195					200					205							
Leu	Gln	Val	Ile	Ala	Ser	Thr	Thr	Lys	Gly	Ile	Asp	Phe	Leu	Glu	Phe				
	210					215					220								
Arg	Pro	Ser	Glu	Ala	Ala	Ala	Ala	Val	Ala	Leu	Ser	Val	Ser	Gly	Glu				
225				230					235						240				
Leu	Gln	Arg	Val	His	Phe	Asp	Asn	Ser	Ser	Phe	Ser	Pro	Leu	Phe	Ser				
			245					250						255					
Leu	Leu	Gln	Lys	Glu	Arg	Val	Lys	Lys	Ile	Gly	Glu	Met	Ile	Glu	Ser				
		260					265						270						
Asp	Gly	Ser	Asp	Leu	Cys	Ser	Gln	Thr	Pro	Asn	Gly	Val	Leu	Glu	Val				
	275						280					285							
Ser	Ala	Cys	Cys	Phe	Ser	Phe	Lys	Thr	His	Asp	Ser	Ser	Ser	Ser	Tyr				
	290					295				300									
Thr	His	Leu	Ser																
305																			

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"
- (iii) HYPOTHETICAL: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAACACTCGA GTGTAATGGC AGAGG

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(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CATCATACTA GTTATAATAA TGTAAG

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